

## SEQUENCE LISTING

<110> Chang, Chawnshang  
 Yi-Fen Lee  
 Wen-Jye Lin

<120> Hydroxyflutamide Induced Pathways  
 Related to Androgen Receptor Negative Prostate Cancer Cells

<130> 21108.0017U2

<140> 10/533,037

<141> 2003-10-31

<150> PCT/US03/34636

<151> 2003-10-31

<150> 60/423,340

<151> 2002-10-31

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1587

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 1

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ctgaaagtcc	atctgctgca	tcggtcaaga	gaaactccac	ttgcatgaag	attgcacgcc	180
tgcagcttgc	atctttgttg	caaaactagc	tacagaagag	aagcaaggca	aagtcttttg	240
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accctggcct	taaaattcca	aaagaagcat	ttgaacaacc	tcagaccagt	tccacaccac	360
ctagagattt	agactccaag	gcttgcatth	ctattggaaa	tcagaacttt	gaggtgaagg	420
cagatgacct	ggagcctata	atggaactgg	gacgaggtgc	gtacgggggtg	gtggagaaga	480
tgcggcacgt	gcccagcggg	cagatcatgg	cagtgaagcg	gatccgagcc	acagtaaata	540
gccaggaaca	gaaacggcta	ctgatggatt	tggatatttc	catgaggacg	gtggactgtc	600
cattcactgt	caccttttat	ggcgactgt	ttcgggaggg	tgatgtgtgg	atctgcatgg	660
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tcgggtcaagt	gaagatgtgc	gattttggaa	tcagtggcta	cttggtggac	tctgttgcta	900
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accagaaggg	atacagtgtg	aagtctgaca	tttgaggtct	gggcatcacg	atgattgagt	1020
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aacatccatt	tttcacccta	catgaatcca	aagggaacaga	tgtggcatct	tttgtaaaac	1260

tgattcttgg	agactaaaaa	gcagtggact	taatcggttg	accctactgt	ggattgggtgg	1320
gtttcggggg	gaagcaagtt	cactacagca	tcaatagaaa	gtcatctttg	agataattta	1380
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ccttggaaatc tatagtatatg aatgaactgt ctagatggat gaattatgat aaaggcttag      1500
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<210> 2
<211> 334
<212> PRT
<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

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 20          25          30
Leu Asp Ser Lys Ala Cys Ile Ser Ile Gly Asn Gln Asn Phe Glu Val
 35          40          45
Lys Ala Asp Asp Leu Glu Pro Ile Met Glu Leu Gly Arg Gly Ala Tyr
 50          55          60
Gly Val Val Glu Lys Met Arg His Val Pro Ser Gly Gln Ile Met Ala
 65          70          75          80
Val Lys Arg Ile Arg Ala Thr Val Asn Ser Gln Glu Gln Lys Arg Leu
 85          90          95
Leu Met Asp Leu Asp Ile Ser Met Arg Thr Val Asp Cys Pro Phe Thr
100          105          110
Val Thr Phe Tyr Gly Ala Leu Phe Arg Glu Gly Asp Val Trp Ile Cys
115          120          125
Met Glu Leu Met Asp Thr Ser Leu Asp Lys Phe Tyr Lys Gln Val Ile
130          135          140
Asp Lys Gly Gln Thr Ile Pro Glu Asp Ile Leu Gly Lys Ile Ala Val
145          150          155          160
Ser Ile Val Lys Ala Leu Glu His Leu His Ser Lys Leu Ser Val Ile
165          170          175
His Arg Asp Val Lys Pro Ser Asn Val Leu Ile Asn Ala Leu Gly Gln
180          185          190
Val Lys Met Cys Asp Phe Gly Ile Ser Gly Tyr Leu Val Asp Ser Val
195          200          205
Ala Lys Thr Ile Asp Ala Gly Cys Lys Pro Tyr Met Ala Pro Glu Arg
210          215          220

Ile Asn Pro Glu Leu Asn Gln Lys Gly Tyr Ser Val Lys Ser Asp Ile
225          230          235          240
Trp Ser Leu Gly Ile Thr Met Ile Glu Leu Ala Ile Leu Arg Phe Pro
245          250          255
Tyr Asp Ser Trp Gly Thr Pro Phe Gln Gln Leu Lys Gln Val Val Glu
260          265          270
Glu Pro Ser Pro Gln Leu Pro Ala Asp Lys Phe Ser Ala Glu Phe Val
275          280          285
Asp Phe Thr Ser Gln Cys Leu Lys Lys Asn Ser Lys Glu Arg Pro Thr
290          295          300
Tyr Pro Glu Leu Met Gln His Pro Phe Phe Thr Leu His Glu Ser Lys
305          310          315          320
Gly Thr Asp Val Ala Ser Phe Val Lys Leu Ile Leu Gly Asp
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<211> 3080

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&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 3

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ggggaagggtg	ctcacgctcg	tgtgcagacc	tgtgtcaatc	tcatacccaa	ccaggaatat	240
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gagatgctgt	accagtgcc	gggacatagg	aatgttctag	aactgattga	gttcttttag	360
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atccatagaa	ggcgccactt	taacgagctg	gaggccagcg	tggtagtaca	ggacgtggcc	480
agtgccttgg	acttctctga	taacaaaggc	atcgcccaca	gggacctaaa	gccagagaac	540
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&lt;210&gt; 4

&lt;211&gt; 412

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 4

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Glu	Asp	Val	Tyr	Gln	Leu	Gln	Glu	Asp	Val	Leu	Gly	Glu	Gly	Ala	His	35	40	45	
Ala	Arg	Val	Gln	Thr	Cys	Val	Asn	Leu	Ile	Thr	Asn	Gln	Glu	Tyr	Ala	50	55	60	
Val	Lys	Ile	Ile	Glu	Lys	Gln	Leu	Gly	His	Ile	Arg	Ser	Arg	Val	Phe	65	70	75	80
Arg	Glu	Val	Glu	Met	Leu	Tyr	Gln	Cys	Gln	Gly	His	Arg	Asn	Val	Leu	85	90	95	
Glu	Leu	Ile	Glu	Phe	Phe	Glu	Glu	Glu	Asp	Arg	Phe	Tyr	Leu	Val	Phe	100	105	110	
Glu	Lys	Met	Arg	Gly	Gly	Ser	Ile	Leu	Ser	His	Ile	His	Arg	Arg	Arg	115	120	125	
His	Phe	Asn	Glu	Leu	Glu	Ala	Ser	Val	Val	Val	Gln	Asp	Val	Ala	Ser	130	135	140	
Ala	Leu	Asp	Phe	Leu	His	Asn	Lys	Gly	Ile	Ala	His	Arg	Asp	Leu	Lys	145	150	155	160
Pro	Glu	Asn	Ile	Leu	Cys	Glu	His	Pro	Asn	Gln	Val	Ser	Pro	Val	Lys	165	170	175	
Ile	Cys	Asp	Phe	Asp	Leu	Gly	Ser	Gly	Ile	Lys	Leu	Asn	Gly	Asp	Cys	180	185	190	
Ser	Pro	Ile	Ser	Thr	Pro	Glu	Leu	Leu	Thr	Pro	Cys	Gly	Ser	Ala	Glu	195	200	205	
Tyr	Met	Ala	Pro	Glu	Val	Val	Glu	Ala	Phe	Ser	Glu	Glu	Ala	Ser	Ile	210	215	220	
Tyr	Asp	Lys	Arg	Cys	Asp	Leu	Trp	Ser	Leu	Gly	Val	Ile	Leu	Tyr	Ile	225	230	235	240
Leu	Leu	Ser	Gly	Tyr	Pro	Pro	Phe	Val	Gly	His	Cys	Gly	Ser	Asp	Cys	245	250	255	
Gly	Trp	Asp	Arg	Gly	Glu	Ala	Cys	Pro	Ala	Cys	Gln	Asn	Met	Leu	Phe	260	265	270	
Glu	Ser	Ile	Gln	Glu	Gly	Lys	Tyr	Glu	Phe	Pro	Asp	Lys	Asp	Trp	Ser	275	280	285	
His	Ile	Ser	Phe	Ala	Ala	Lys	Asp	Leu	Ile	Ser	Lys	Leu	Leu	Val	Arg	290	295	300	
Asp	Ala	Lys	Gln	Arg	Leu	Ser	Ala	Ala	Gln	Val	Leu	Gln	His	Pro	Trp	305	310	315	320
Val	Gln	Gly	Cys	Ala	Pro	Glu	Asn	Thr	Leu	Pro	Thr	Pro	Leu	Val	Leu	325	330	335	
Gln	Arg	Asn	Ser	Cys	Ala	Lys	Asp	Leu	Thr	Ser	Phe	Ala	Ala	Glu	Ala	340	345	350	
Ile	Ala	Met	Asn	Arg	Gln	Leu	Ala	Gln	Cys	Glu	Glu	Asp	Ala	Gly	Gln	355	360	365	
Asp	Gln	Pro	Val	Val	Ile	Arg	Ala	Thr	Ser	Arg	Cys	Leu	Gln	Leu	Ser	370	375	380	
Pro	Pro	Ser	Gln	Ser	Lys	Leu	Ala	Gln	Arg	Arg	Gln	Arg	Ala	Ser	Leu	385	390	395	400

Ser Ala Thr Pro Val Val Leu Val Gly Asp Arg Ala  
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<210> 5  
<211> 1096  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

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cttcttgctc agtgccctga agtttctctg caatgaactg acaaatcgga accatggtgc 180  
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gcagtgcacag tgtggctcag actcctgagc tgctgcggag gtaccacta gaggatcacc 300  
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<210> 6  
<211> 232  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:/note =  
synthetic construct

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Val Gly Ala Arg His Pro Ser Ser Asp Ser Val Ala Gln Thr Pro Glu  
20 25 30  
Leu Leu Arg Arg Tyr Pro Leu Glu Asp His Pro Glu Phe Pro Leu Pro  
35 40 45  
Pro Asp Val Val Phe Phe Cys Gln Pro Glu Gly Cys Leu Ser Val Arg  
50 55 60  
Gln Arg Arg Met Ser Leu Arg Asp Asp Thr Ser Phe Val Phe Thr Leu  
65 70 75 80  
Thr Asp Lys Asp Thr Gly Val Thr Arg Tyr Gly Ile Cys Val Asn Phe  
85 90 95  
Tyr Arg Ser Phe Gln Lys Arg Met Pro Lys Glu Lys Val Glu Gly Gly  
100 105 110  
Ala Gly Pro Arg Gly Lys Glu Gly Ala His Thr Ser Gly Ala Ser Glu  
115 120 125

Glu	Ala	Ala	Ala	Gly	Ser	Ser	Glu	Ser	Gly	Ser	Thr	Leu	Gln	Pro	Pro
130						135					140				
Ser	Ala	Asp	Ser	Thr	Pro	Asp	Val	Asn	Gln	Ser	Pro	Arg	Gly	Lys	Arg
145					150					155					160
Arg	Ala	Lys	Ala	Gly	Ser	Arg	Ser	Arg	Asn	Ser	Thr	Leu	Thr	Ser	Leu
				165					170					175	
Cys	Val	Leu	Ser	His	Tyr	Pro	Phe	Phe	Ser	Thr	Phe	Arg	Glu	Cys	Leu
			180					185					190		
Tyr	Thr	Leu	Lys	Arg	Leu	Val	Asp	Cys	Cys	Ser	Glu	Arg	Leu	Leu	Gly
	195						200					205			
Lys	Lys	Leu	Gly	Ile	Pro	Arg	Gly	Val	Gln	Arg	Tyr	Gly	Leu	Leu	Leu
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Val	Leu	Gly	Arg	Thr	Leu	Arg	Asp								
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<210> 7

<211> 7161

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 7

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agggggccga	gcgaatgtag	cccgcgagag	aaaatggcgg	cggcggcggg	gaatcgcgcc	180
tcgtcgctcg	gattcccggg	cgccagggtc	acgagccctg	aggcaggcgg	cggcggagga	240
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&lt;210&gt; 8

&lt;211&gt; 1563

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 8

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Trp Pro Asp Pro Ala Gly Lys Lys Asp Val Arg Arg Glu Ala Ser Asp
          20           25           30
Ser Gly Arg Ala Gly Thr Trp Pro Arg Gly Pro Ser Glu Cys Ser Pro
          35           40           45
Arg Glu Lys Met Ala Ala Ala Gly Asn Arg Ala Ser Ser Ser Gly
          50           55           60
Phe Pro Gly Ala Arg Ala Thr Ser Pro Glu Ala Gly Gly Gly Gly Gly
65           70           75           80
Ala Leu Lys Ala Ser Ser Ala Pro Ala Ala Ala Gly Leu Leu Arg
          85           90           95
Glu Ala Gly Ser Gly Gly Arg Glu Arg Ala Asp Trp Arg Arg Arg Gln
          100          105          110

Leu Arg Lys Val Arg Ser Val Glu Leu Asp Gln Leu Pro Glu Gln Pro
          115          120          125
Leu Phe Leu Ala Ala Ser Pro Pro Ala Ser Ser Thr Ser Pro Ser Pro
          130          135          140
Glu Pro Ala Asp Ala Ala Gly Ser Gly Thr Gly Phe Gln Pro Val Ala
145          150          155          160
Val Pro Pro Pro His Gly Ala Ala Ser Arg Gly Gly Ala His Leu Thr
          165          170          175

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Glu	Ser	Val	Ala	Ala	Pro	Asp	Ser	Gly	Ala	Ser	Ser	Pro	Ala	Ala	Ala			
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Glu	Pro	Gly	Glu	Lys	Arg	Ala	Pro	Ala	Ala	Glu	Pro	Ser	Pro	Ala	Ala			
			195					200					205					
Ala	Pro	Ala	Gly	Arg	Glu	Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu			
			210				215					220						
His	Lys	Met	Asp	Asp	Arg	Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu			
			225				230					235			240			
Lys	Ala	Thr	Cys	Met	Pro	Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Arg			
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Asn	Arg	Arg	Gly	Pro	Val	Val	Val	Lys	Pro	Ile	Pro	Val	Lys	Gly	Asp			
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Gly	Ser	Glu	Met	Asn	His	Leu	Ala	Ala	Glu	Ser	Pro	Gly	Glu	Val	Gln			
			275				280					285						
Ala	Ser	Ala	Ala	Ser	Pro	Ala	Ser	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro			
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Gly	Asn	Ser	Pro	Ser	Gly	Arg	Thr	Val	Lys	Ser	Glu	Ser	Pro	Gly	Val			
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Pro	Pro	Arg	Arg	Ala	Pro	Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro			
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Glu	Glu	Thr	Asn	Arg	Arg	Val	Asn	Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr			
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Leu	Leu	Gln	Gln	Ile	Gly	Pro	Asn	Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser			
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Pro	Asp	Asn	Lys	Tyr	Arg	Val	Phe	Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys			
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Ala	Arg	Gly	Thr	Phe	Cys	Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val			
				405						410				415				
Phe	Gln	Leu	Glu	Pro	Ser	Asp	Pro	Met	Leu	Trp	Arg	Lys	Thr	Leu	Lys			
				420				425					430					
Asn	Phe	Glu	Val	Glu	Ser	Leu	Phe	Gln	Lys	Tyr	His	Ser	Arg	Arg	Ser			
			435				440					445						
Ser	Arg	Ile	Lys	Ala	Pro	Ser	Arg	Asn	Thr	Ile	Gln	Lys	Phe	Val	Ser			
			450				455					460						
Arg	Met	Ser	Asn	Ser	His	Thr	Leu	Ser	Ser	Ser	Ser	Thr	Ser	Thr	Ser			
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Ser	Ser	Glu	Asn	Ser	Ile	Lys	Asp	Glu	Glu	Glu	Gln	Met	Cys	Pro	Ile			
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Cys	Leu	Leu	Gly	Met	Leu	Asp	Glu	Glu	Ser	Leu	Thr	Val	Cys	Glu	Asp			
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Gly	Cys	Arg	Asn	Lys	Leu	His	His	Cys	Met	Ser	Ile	Trp	Ala	Glu				
			515				520					525						
Glu	Cys	Arg	Arg	Asn	Arg	Glu	Pro	Leu	Ile	Cys	Pro	Leu	Cys	Arg	Ser			
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Lys	Trp	Arg	Ser	His	Asp	Phe	Tyr	Ser	His	Glu	Leu	Ser	Ser	Pro	Val			
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Asp	Ser	Pro	Ser	Ser	Leu	Arg	Ala	Ala	Gln	Gln	Gln	Thr	Val	Gln	Gln			
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Gln	Pro	Leu	Ala	Gly	Ser	Arg	Arg	Asn	Gln	Glu	Ser	Asn	Phe	Asn	Leu			
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Thr	His	Tyr	Gly	Thr	Gln	Gln	Ile	Pro	Pro	Ala	Tyr	Lys	Asp	Leu	Ala			
			595				600					605						
Glu	Pro	Trp	Ile	Gln	Val	Phe	Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe			
			610				615					620						
Ser	Arg	Asn	Trp	Asn	Val	Arg	Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His			
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Ala	Leu	Lys	Thr	Leu	Arg	Ala	Met	Leu	Val	Tyr	Thr	Pro	Cys	His	Ser	
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	770					775					780					
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 Glu Lys Cys Arg Leu Asp Val Asn Thr Glu Leu Asn Ser Ser Ile Glu  
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 Thr Tyr Lys Asp Asp Val Asn His Asn Gln Lys Cys Lys Glu Lys Met  
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 Leu Arg Cys Leu Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu  
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&lt;211&gt; 3621

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 9

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<210> 10

<211> 657

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 10

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Asn Lys Asp Thr Gly His Ser Asn Arg Gln Lys Lys His Asn Ser Ser
          35           40           45
Ser Ser Ala Leu Leu Asn Ser Pro Thr Val Thr Thr Ser Ser Cys Ala
          50           55           60
Gly Ala Ser Glu Lys Lys Lys Phe Leu Ser Asp Val Arg Ile Lys Phe
65          70          75          80
Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val Lys
          85          90          95
Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro Leu
          100         105         110
Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn Gln
          115         120         125
Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser Met
          130         135         140
Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn Ser
          145         150         155         160
Ser Ser Pro His Ser Gly Val Ser Arg Gln Val Arg Ile Lys Ala Ser
          165         170         175
Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro Arg
          180         185         190
Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser Pro
          195         200         205
Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln Gly
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Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr Ser
          225         230         235         240
Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu Ser
          245         250         255

Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe Arg
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Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln Glu
          275         280         285
Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly Gly
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Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr Ser
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 Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg Ser  
 355 360 365  
 Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro Thr  
 370 375 380  
 Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu Gly  
 385 390 395 400  
 Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr Gly  
 405 410 415  
 Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro Glu  
 420 425 430  
 Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu Lys  
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 Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg Asp  
 450 455 460  
 Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly Gly  
 465 470 475 480  
 Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser Val  
 485 490 495  
 Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu His  
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 Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu Arg  
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 Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys Arg  
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 Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr Gly  
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 Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr Gly  
 565 570 575  
 Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met Leu  
 580 585 590  
 Thr Glu Lys Pro Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile Phe  
 595 600 605  
 Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile Ser  
 610 615 620  
 Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg Gln  
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<210> 11

<211> 3336

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 11

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&lt;211&gt; 544

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 12

16



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<210> 13  
 <211> 444  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 13

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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

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&lt;210&gt; 15

&lt;211&gt; 1495

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 15

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Ala	Arg	Ala	Ala	Ala	Ala	Gly	Leu	Leu	Arg	Glu	Ala	Gly	Ser	Gly	Gly	20	25	30	
Arg	Glu	Arg	Ala	Asp	Trp	Arg	Arg	Gln	Leu	Arg	Lys	Val	Arg	Ser		35	40	45	
Val	Glu	Leu	Asp	Gln	Leu	Pro	Glu	Gln	Pro	Leu	Phe	Leu	Ala	Ala	Ser	50	55	60	
Pro	Pro	Ala	Ser	Ser	Thr	Ser	Pro	Ser	Pro	Glu	Pro	Ala	Asp	Ala	Ala	65	70	75	80
Gly	Ser	Gly	Thr	Gly	Phe	Gln	Pro	Val	Ala	Val	Pro	Pro	Pro	His	Gly	85	90	95	
Ala	Ala	Ser	Arg	Arg	Gly	Ala	His	Leu	Thr	Glu	Ser	Val	Ala	Ala	Pro	100	105	110	
Asp	Ser	Gly	Ala	Ser	Ser	Pro	Ala	Ala	Ala	Glu	Pro	Gly	Glu	Lys	Arg	115	120	125	
Ala	Pro	Ala	Ala	Glu	Pro	Ser	Pro	Ala	Ala	Ala	Pro	Ala	Gly	Arg	Glu	130	135	140	
Met	Glu	Asn	Lys	Glu	Thr	Leu	Lys	Gly	Leu	His	Lys	Met	Asp	Asp	Arg	145	150	155	160
Pro	Glu	Glu	Arg	Met	Ile	Arg	Glu	Lys	Leu	Lys	Ala	Thr	Cys	Met	Pro	165	170	175	
Ala	Trp	Lys	His	Glu	Trp	Leu	Glu	Arg	Asn	Arg	Arg	Gly	Pro	Val		180	185	190	
Val	Val	Lys	Pro	Ile	Pro	Val	Lys	Gly	Asp	Gly	Ser	Glu	Met	Asn	His	195	200	205	
Leu	Ala	Ala	Glu	Ser	Pro	Gly	Glu	Val	Gln	Ala	Ser	Ala	Ala	Ser	Pro	210	215	220	
Ala	Ser	Lys	Gly	Arg	Arg	Ser	Pro	Ser	Pro	Gly	Asn	Ser	Pro	Ser	Gly	225	230	235	240
Arg	Thr	Val	Lys	Ser	Glu	Ser	Pro	Gly	Val	Arg	Arg	Lys	Arg	Val	Ser	245	250	255	
Pro	Val	Pro	Phe	Gln	Ser	Gly	Arg	Ile	Thr	Pro	Pro	Arg	Arg	Ala	Pro	260	265	270	
Ser	Pro	Asp	Gly	Phe	Ser	Pro	Tyr	Ser	Pro	Glu	Glu	Thr	Asn	Arg	Arg	275	280	285	
Val	Asn	Lys	Val	Met	Arg	Ala	Arg	Leu	Tyr	Leu	Leu	Gln	Gln	Ile	Gly	290	295	300	
Pro	Asn	Ser	Phe	Leu	Ile	Gly	Gly	Asp	Ser	Pro	Asp	Asn	Lys	Tyr	Arg	305	310	315	320
Val	Phe	Ile	Gly	Pro	Gln	Asn	Cys	Ser	Cys	Ala	His	Gly	Thr	Phe	Cys	325	330	335	
Ile	His	Leu	Leu	Phe	Val	Met	Leu	Arg	Val	Phe	Gln	Leu	Glu	Pro	Ser	340	345	350	
Asp	Pro	Met	Leu	Trp	Arg	Lys	Thr	Leu	Lys	Asn	Phe	Glu	Val	Glu	Ser	355	360	365	
Leu	Phe	Gln	Lys	Tyr	His	Ser	Arg	Arg	Ser	Ser	Arg	Ile	Lys	Ala	Pro	370	375	380	
Ser	Arg	Asn	Thr	Ile	Gln	Lys	Phe	Val	Ser	Arg	Met	Ser	Asn	Ser	His	385	390	395	400
Thr	Leu	Ser	Ser	Ser	Ser	Thr	Ser	Thr	Ser	Ser	Ser	Glu	Asn	Ser	Ile	405	410	415	
Lys	Asp	Glu	Glu	Glu	Gln	Met	Cys	Pro	Ile	Cys	Leu	Leu	Gly	Met	Leu	420	425	430	

Asp	Glu	Glu	Ser	Leu	Thr	Val	Cys	Glu	Asp	Gly	Cys	Arg	Asn	Lys	Leu	435	440	445
His	His	His	Cys	Met	Ser	Ile	Trp	Ala	Glu	Glu	Cys	Arg	Arg	Asn	Arg	450	455	460
Glu	Pro	Leu	Ile	Cys	Pro	Leu	Cys	Arg	Ser	Lys	Trp	Arg	Ser	His	Asp	465	470	475
Phe	Tyr	Ser	His	Glu	Leu	Ser	Ser	Pro	Val	Asp	Ser	Pro	Ser	Ser	Leu	485	490	495
Arg	Ala	Ala	Gln	Gln	Gln	Thr	Val	Gln	Gln	Gln	Pro	Leu	Ala	Gly	Ser	500	505	510
Arg	Arg	Asn	Gln	Glu	Ser	Asn	Phe	Asn	Leu	Thr	His	Tyr	Gly	Thr	Gln	515	520	525
Gln	Ile	Pro	Pro	Ala	Tyr	Lys	Asp	Leu	Ala	Glu	Pro	Trp	Ile	Gln	Val	530	535	540
Phe	Gly	Met	Glu	Leu	Val	Gly	Cys	Leu	Phe	Ser	Arg	Asn	Trp	Asn	Val	545	550	555
Arg	Glu	Met	Ala	Leu	Arg	Arg	Leu	Ser	His	Asp	Val	Ser	Gly	Ala	Leu	565	570	575
Leu	Leu	Ala	Asn	Gly	Glu	Ser	Thr	Gly	Asn	Ser	Gly	Gly	Ser	Ser	Gly	580	585	590
Ser	Ser	Pro	Ser	Gly	Gly	Ala	Thr	Ser	Gly	Ser	Ser	Gln	Thr	Ser	Ile	595	600	605
Ser	Gly	Asp	Val	Val	Glu	Ala	Cys	Cys	Ser	Val	Leu	Ser	Met	Val	Cys	610	615	620
Ala	Asp	Pro	Val	Tyr	Lys	Val	Tyr	Val	Ala	Ala	Leu	Lys	Thr	Leu	Arg	625	630	635
Ala	Met	Leu	Val	Tyr	Thr	Pro	Cys	His	Ser	Leu	Ala	Glu	Arg	Ile	Lys	645	650	655
Leu	Gln	Arg	Leu	Leu	Gln	Pro	Val	Val	Asp	Thr	Ile	Leu	Val	Lys	Cys	660	665	670
Ala	Asp	Ala	Asn	Ser	Arg	Thr	Ser	Gln	Leu	Ser	Ile	Ser	Thr	Leu	Leu	675	680	685
Glu	Leu	Cys	Lys	Gly	Gln	Ala	Gly	Glu	Leu	Ala	Val	Gly	Arg	Glu	Ile	690	695	700
Leu	Lys	Ala	Gly	Ser	Ile	Gly	Ile	Gly	Gly	Val	Asp	Tyr	Val	Leu	Asn	705	710	715
Cys	Ile	Leu	Gly	Asn	Gln	Thr	Glu	Ser	Asn	Asn	Trp	Gln	Glu	Leu	Leu	725	730	735
Gly	Arg	Leu	Cys	Leu	Ile	Asp	Arg	Leu	Leu	Leu	Glu	Phe	Pro	Ala	Glu	740	745	750
Phe	Tyr	Pro	His	Ile	Val	Ser	Thr	Asp	Val	Ser	Gln	Ala	Glu	Pro	Val	755	760	765
Glu	Ile	Arg	Tyr	Lys	Lys	Leu	Leu	Ser	Leu	Leu	Thr	Phe	Ala	Leu	Gln	770	775	780
Ser	Ile	Asp	Asn	Ser	His	Ser	Met	Val	Gly	Lys	Leu	Ser	Arg	Arg	Ile	785	790	795
Tyr	Leu	Ser	Ser	Ala	Arg	Met	Val	Thr	Thr	Val	Pro	His	Val	Phe	Ser	805	810	815
Lys	Leu	Leu	Glu	Met	Leu	Ser	Val	Ser	Ser	Val	Ser	Thr	His	Phe	Thr	820	825	830
Arg	Met	Arg	Arg	Arg	Leu	Met	Ala	Tyr	Ala	Asp	Glu	Val	Glu	Ile	Ala	835	840	845
Glu	Ala	Ile	Gln	Leu	Gly	Val	Glu	Asp	Thr	Leu	Gln	Arg	Gln	Gln	His	850	855	860
Asn	Ser	Phe	Cys	Arg	His	Leu	Phe	Pro	Thr	Thr	Ile	Trp	Lys	Pro	Gln	865	870	875
Arg	Thr	Val	Pro	Leu	Glu	Cys	Thr	Val	His	Leu	Glu	Lys	Thr	Gly	Lys	885	890	895
Gly	Leu	Cys	Ala	Thr	Lys	Leu	Ser	Ala	Ser	Ser	Glu	Asp	Ile	Ser	Glu	900	905	910

Arg Leu Ala Arg Ile Ser Val Gly Pro Ser Ser Ser Thr Thr Thr Thr  
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 Thr Thr Thr Thr Glu Gln Pro Lys Pro Met Val Gln Thr Lys Gly Arg  
 930 935 940  
 Pro His Ser Gln Cys Leu Asn Ser Ser Pro Leu Ser His His Ser Gln  
 945 950 955 960  
 Leu Met Phe Pro Ala Leu Ser Thr Pro Ser Ser Ser Thr Pro Ser Val  
 965 970 975  
 Pro Ala Gly Thr Ala Thr Asp Val Ser Lys His Arg Leu Gln Gly Phe  
 980 985 990  
 Ile Pro Cys Arg Ile Pro Ser Ala Ser Pro Gln Thr Gln Arg Lys Phe  
 995 1000 1005  
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 His Arg Pro Lys Pro Ser Arg Pro Thr Pro Gly Asn Thr Ser Lys Gln  
 1045 1050 1055  
 Gly Asp Pro Ser Lys Asn Ser Met Thr Leu Asp Leu Asn Ser Ser Ser  
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 Lys Cys Asp Asp Ser Phe Gly Leu Ser Ser Asn Ser Ser Asn Cys Cys  
 1075 1080 1085  
 Tyr Thr Ser Asp Glu Thr Val Phe Thr Pro Val Glu Glu Lys Cys Arg  
 1090 1095 1100  
 Leu Asp Val Asn Thr Glu Leu Asn Ser Ser Ile Glu Asp Leu Leu Glu  
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 Ala Ser Met Pro Ser Ser Asp Thr Thr Val Thr Phe Lys Ser Glu Val  
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 Ala Val Leu Ser Pro Glu Lys Ala Glu Asn Asp Asp Thr Tyr Lys Asp  
 1140 1145 1150  
 Asp Val Asn His Asn Gln Lys Cys Lys Glu Lys Met Glu Ala Glu Glu  
 1155 1160 1165  
  
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 Ile Ile Gln Gln Asp Thr Pro Glu Thr Leu Pro Gly His Thr Lys Ala  
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 Lys Gln Pro Tyr Arg Glu Asp Thr Glu Trp Leu Lys Gly Gln Gln Ile  
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 Gly Leu Gly Ala Phe Ser Ser Cys Tyr Gln Ala Gln Asp Val Gly Thr  
 1235 1240 1245  
 Gly Thr Leu Met Ala Val Lys Gln Val Thr Tyr Val Arg Asn Thr Ser  
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 Ser Glu Gln Glu Glu Val Val Glu Ala Leu Arg Glu Glu Ile Arg Met  
 1265 1270 1275 1280  
 Met Ser His Leu Asn His Pro Asn Ile Ile Arg Met Leu Gly Ala Thr  
 1285 1290 1295  
 Cys Glu Lys Ser Asn Tyr Asn Leu Phe Ile Glu Trp Met Ala Gly Gly  
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 Ser Val Ala His Leu Leu Ser Lys Tyr Gly Ala Phe Lys Glu Ser Val  
 1315 1320 1325  
 Val Ile Asn Tyr Thr Glu Gln Leu Leu Arg Gly Leu Ser Tyr Leu His  
 1330 1335 1340  
 Glu Asn Gln Ile Ile His Arg Asp Val Lys Gly Ala Asn Leu Leu Ile  
 1345 1350 1355 1360  
 Asp Ser Thr Gly Gln Arg Leu Arg Ile Ala Asp Phe Gly Ala Ala Ala  
 1365 1370 1375  
 Arg Leu Ala Ser Lys Gly Thr Gly Ala Gly Glu Phe Gln Gly Gln Leu  
 1380 1385 1390

Leu Gly Thr Ile Ala Phe Met Ala Pro Glu Val Leu Arg Gly Gln Gln  
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 Tyr Gly Arg Ser Cys Asp Val Trp Ser Val Gly Cys Ala Ile Ile Glu  
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 Met Ala Cys Ala Lys Pro Pro Trp Asn Ala Glu Lys His Ser Asn His  
   1425                                  1430                                  1435                                  1440  
 Leu Ala Leu Ile Phe Lys Ile Ala Ser Ala Thr Thr Ala Pro Ser Ile  
                                   1445                                  1450                                  1455  
 Pro Ser His Leu Ser Pro Gly Leu Arg Asp Val Ala Leu Arg Cys Leu  
                                   1460                                  1465                                  1470  
 Glu Leu Gln Pro Gln Asp Arg Pro Pro Ser Arg Glu Leu Leu Lys His  
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<210> 16  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
           synthetic construct

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37

<210> 17  
 <211> 2348  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
           synthetic construct

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 tccagttgct aaagaacttg cagcatgagc gcacgtgca gtactatggc tgtctgcggg 1380  
 accgcgctga gaagaccctg accatcttca tggagtacat gccagggggc tcggtgaaag 1440

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<210> 18

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 18

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Asn Lys Asp Thr Gly His Ser Asn Arg Gln Ser Asp Val Arg Ile Lys
35          40          45
Phe Glu His Asn Gly Glu Arg Arg Ile Ile Ala Phe Ser Arg Pro Val
50          55          60
Lys Tyr Glu Asp Val Glu His Lys Val Thr Thr Val Phe Gly Gln Pro
65          70          75          80
Leu Asp Leu His Tyr Met Asn Asn Glu Leu Ser Ile Leu Leu Lys Asn
85          90          95
Gln Asp Asp Leu Asp Lys Ala Ile Asp Ile Leu Asp Arg Ser Ser Ser
100         105         110
Met Lys Ser Leu Arg Ile Leu Leu Leu Ser Gln Asp Arg Asn His Asn
115         120         125
Ser Ser Ser Pro His Ser Glu Val Ser Arg Gln Val Arg Ile Lys Ala
130         135         140
Ser Gln Ser Ala Gly Asp Ile Asn Thr Ile Tyr Gln Pro Pro Glu Pro
145         150         155         160
Arg Ser Arg His Leu Ser Val Ser Ser Gln Asn Pro Gly Arg Ser Ser
165         170         175
Pro Pro Pro Gly Tyr Val Pro Glu Arg Gln Gln His Ile Ala Arg Gln
180         185         190
Gly Ser Tyr Thr Ser Ile Asn Ser Glu Gly Glu Phe Ile Pro Glu Thr
195         200         205
Ser Glu Gln Cys Met Leu Asp Pro Leu Ser Ser Ala Glu Asn Ser Leu
210         215         220
Ser Gly Ser Cys Gln Ser Leu Asp Arg Ser Ala Asp Ser Pro Ser Phe
225         230         235         240
Arg Lys Ser Arg Met Ser Arg Ala Gln Ser Phe Pro Asp Asn Arg Gln
245         250         255
Glu Tyr Ser Asp Arg Glu Thr Gln Leu Tyr Asp Lys Gly Val Lys Gly
260         265         270

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Gly Thr Tyr Pro Arg Arg Tyr His Val Ser Val His His Lys Asp Tyr  
 275 280 285  
 Ser Asp Gly Arg Arg Thr Phe Pro Arg Ile Arg Arg His Gln Gly Asn  
 290 295 300  
 Leu Phe Thr Leu Val Pro Ser Ser Arg Ser Leu Ser Thr Asn Gly Glu  
 305 310 315 320  
 Asn Met Gly Leu Ala Val Gln Tyr Leu Asp Pro Arg Gly Arg Leu Arg  
 325 330 335  
 Ser Ala Asp Ser Glu Asn Ala Leu Ser Val Gln Glu Arg Asn Val Pro  
 340 345 350  
 Thr Lys Ser Pro Ser Ala Pro Ile Asn Trp Arg Arg Gly Lys Leu Leu  
 355 360 365  
 Gly Gln Gly Ala Phe Gly Arg Val Tyr Leu Cys Tyr Asp Val Asp Thr  
 370 375 380  
 Gly Arg Glu Leu Ala Ser Lys Gln Val Gln Phe Asp Pro Asp Ser Pro  
 385 390 395 400  
 Glu Thr Ser Lys Glu Val Ser Ala Leu Glu Cys Glu Ile Gln Leu Leu  
 405 410 415  
 Lys Asn Leu Gln His Glu Arg Ile Val Gln Tyr Tyr Gly Cys Leu Arg  
 420 425 430  
 Asp Arg Ala Glu Lys Thr Leu Thr Ile Phe Met Glu Tyr Met Pro Gly  
 435 440 445  
 Gly Ser Val Lys Asp Gln Leu Lys Ala Tyr Gly Ala Leu Thr Glu Ser  
 450 455 460  
 Val Thr Arg Lys Tyr Thr Arg Gln Ile Leu Glu Gly Met Ser Tyr Leu  
 465 470 475 480  
 His Ser Asn Met Ile Val His Arg Asp Ile Lys Gly Ala Asn Ile Leu  
 485 490 495  
 Arg Asp Ser Ala Gly Asn Val Lys Leu Gly Asp Phe Gly Ala Ser Lys  
 500 505 510  
 Arg Leu Gln Thr Ile Cys Met Ser Gly Thr Gly Met Arg Ser Val Thr  
 515 520 525  
 Gly Thr Pro Tyr Trp Met Ser Pro Glu Val Ile Ser Gly Glu Gly Tyr  
 530 535 540  
 Gly Arg Lys Ala Asp Val Trp Ser Leu Gly Cys Thr Val Val Glu Met  
 545 550 555 560  
 Leu Thr Glu Lys Pro Trp Ala Glu Tyr Glu Ala Met Ala Ala Ile  
 565 570 575  
 Phe Lys Ile Ala Thr Gln Pro Thr Asn Pro Gln Leu Pro Ser His Ile  
 580 585 590  
 Ser Glu His Gly Arg Asp Phe Leu Arg Arg Ile Phe Val Glu Ala Arg  
 595 600 605  
 Gln Arg Pro Ser Ala Glu Glu Leu Leu Thr His His Phe Ala Gln Leu  
 610 615 620  
 Met Tyr  
 625

<210> 19

<211> 1576

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 19

gaattcgagc	cgaccgaccg	ctcccggccc	gccccctatg	ggccccggct	agaggcgccg	60
ccgccgcccg	cccgcggagc	cccgatgctg	gcccggagga	agccgggtgct	gccggcgctc	120
accatcaacc	ctaccatcgc	cgagggccca	tcccctacca	gcgagggcgc	ctccgaggca	180



aacctggtgg	acctgcagaa	gaagctggag	gagctggaac	ttgacgagca	gcagaagaag	240
cggctggaag	cctttctcac	ccagaaagcc	aagggtggcg	aactcaaaga	cgatgacttc	300
gaaaggatct	cagagctggg	cgcgggcaac	ggcgggggag	tcaccaaagt	ccagcacaga	360
ccctcggggc	tcatcatggc	caggaagctg	atccaccttg	agatcaagcc	ggccatccgg	420
aaccagatca	tccgcgagct	gcaggtcctg	cacgaatgca	actcgccgta	catcgtgggc	480
ttctacgggg	ccttctacag	tgacggggag	atcagcattt	gcattggaaca	catggacggc	540
ggctccctgg	accagggtgt	gaaagaggcc	aagaggattc	ccgaggagat	cctggggaaa	600
gtcagcatcg	cggttctccg	gggcttggcg	tacctccgag	agaagcacca	gatcatgcac	660
cgagatgtga	agccctccaa	catcctcgtg	aactctagag	gggagatcaa	gctgtgtgac	720
ttcgggggtga	gcggccagct	catagactcc	atggccaact	ccttcgtggg	cacgcgtctc	780
tacatggctc	cggagcgggt	gcagggcaca	cattactcgg	tgacgtcgga	catctggagc	840
atgggctgtg	ccctggtgga	gctggccgtc	ggaaggtagc	ccatcccccc	gcccagcgcc	900
aaagagctgg	aggccatctt	tggccggccc	gtggtcgacg	gggaagaagg	agagcctcac	960
agcatctcgc	ctcggccgag	gccccccggg	cgccccgtca	gcggtcacgg	gatggatagc	1020
cggcctgcca	tggccatctt	tgaactcctg	gactatattg	tgaacgagcc	acctcctaag	1080
ctgcccacacg	gtgtgttcac	ccccgacttc	caggagtttg	tcaataaatg	cctcatcaag	1140
aaccacagcgg	agcgggcgga	cctgaagatg	ctcacaaaacc	acaccttcac	caagcgggtc	1200
gaggtggaag	aagtggattt	tgccggctgg	ttgtgtaaaa	ccctgcggct	gaaccagccc	1260
ggcacaccca	cgcgcaccgc	cgtgtgacag	tggccgggct	ccctgcgtcc	cgctggtgac	1320
ctgcccacccg	tccctgtcca	tgccccgccc	tccagctga	ggacacgtgg	cgctccacc	1380
caccttcctg	cctcacccctg	cggagagcac	cgtggcgggg	cgacagcgca	tgacgaaacg	1440
gggggtctct	ctcctgccag	tcctggccgg	ggtgcctctg	gggacgggcg	acgctgctgt	1500
gtgtggtctc	agaggctctg	cttccttagg	ttacaaaaca	aaacaggggag	agaaaagcaa	1560
aaaaaaaaaa	aaaaaa					1576

&lt;210&gt; 20

&lt;211&gt; 2222

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 20

attcggcacg	agggaggaag	cgagaggtgc	tgccctcccc	ccggagttgg	aagcgcgtta	60
cccgggtcca	aaatgcccac	gaagaagccg	acgcccatac	agctgaaccc	ggcccccgac	120
ggctctgcag	ttaacgggac	cagctctcgc	gagaccaact	tggaggcctt	gcagaagaag	180
ctggaggagc	tagagcttga	tgagcagcag	cgaagcgcc	ttgaggcctt	tcttaccag	240
aagcagaagg	tgggagaact	gaaggatgac	gactttgaga	agatcagtga	gctgggggct	300
ggcaatggcg	gtgtggtgtt	caaggtctcc	cacaagcctt	ctggcctggt	catggccaga	360
aagctaattc	atctggagat	caaaccgcga	atccggaaac	agatcataag	ggagctgcag	420
gttctgcatg	agtgcactc	tccgtacatc	gtgggcttct	atggtgcgtt	ctacagcgat	480
ggcgagatca	gtatctgcat	ggagcacatg	gatggagggt	ctctggatca	agtccctgaag	540
aaagctggaa	gaattcctga	acaaatttta	ggaaaagtta	gcattgctgt	aataaaaaggc	600
ctgacataatc	tgaggggagaa	gcacaagatc	atgcacagag	atgtcaagcc	ctccaacatc	660
ctagtcaact	cccgtgggga	gatcaagctc	tgtgactttg	gggtcagcgg	gcagctcatc	720
gactccatgg	ccaactcctt	cgtgggcaca	aggtcctaca	tgtcgccaga	aagactccag	780
gggactcatt	actctgtgca	gtcagacatc	tggagcatgg	gactgtctct	ggtagagatg	840
gcggttggga	ggtatcccat	ccctcctcca	gatgccaagg	agctggagct	gatgtttggg	900
tgccagggtgg	aaggagatgc	ggctgagacc	ccaccagggc	caaggacccc	cgggaggccc	960
cttagctcat	acggaatgga	cagccgacct	cccattggcaa	tttttgagtt	gttggtattac	1020
atagtcaacg	agcctcctcc	aaaactgccc	agtggagtgt	tcagtctgga	atttcaagat	1080
tttctgaata	aatgcttaat	aaaaaacccc	gcagagagag	cagatttgaa	gcaactcatg	1140
gttcatgctt	ttatcaagag	atctgatgct	gaggaagtgg	attttgcagg	ttggctctgc	1200
tccaccatcg	gccttaacca	gcccagcaca	ccaaccatg	ctgctggcgt	ctaagtgttt	1260
gggaagcaac	aaagagcgag	tcccctgccc	ggtggtttgc	catgtcgctt	ttgggcctcc	1320
ttcccatgcc	tgtctctgtt	cagatgtgca	tttcacctgt	gacaaaggat	gaagaacaca	1380
gcattgtgcca	agattctact	cttgtcattt	ttaatattac	tgtctttatt	cttattacta	1440
ttattgttcc	cctaagtgga	ttggctttgt	gcttggggct	atttgtgtgt	atgctgatga	1500
tcaaaacctg	tgccaggctg	aattacagtg	aaatttttgg	tgaatgtggg	tagtcattct	1560

tacaattgca	ctgctgttcc	tgctccatga	ctggctgtct	gcctgtatct	tcggactttg	1620
acatttgaca	tttggtggac	tttatcttgc	tgggcatact	ttctctctag	gagggagcct	1680
tgtgagatcc	ttcacaggca	gtgcatgtga	agcatgcttt	gctgctatga	aatgagcat	1740
cagagagtgt	acatcatgtt	attttattat	tattatttgc	ttttcatgta	gaactcagca	1800
gttgacatcc	aaatctagcc	agagcccttc	actgccatga	tagctggggc	ttcaccagtc	1860
tgtctactgt	ggtgatctgt	agacttctgg	ttgtatttct	atatttattt	tcagtatact	1920
gtgtgggata	cttagtggtg	tgtctcttta	agttttgatt	aatgtttctt	aaatggaatt	1980
atgtgaatgt	cacaaattga	tcaagatatt	aaaatgtcgg	atztatcttt	ccccatatcc	2040
aagtaccaat	gctgttgtaa	acaacgtgta	tagtgccata	aattgtatga	aaatcctttt	2100
aaccatttta	acctagatgt	ttaacaaatc	taatctctta	ttctaataaa	tatactatga	2160
aataaaaaaa	aaaggagaaa	gctaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	aaaaaaaaaa	2220
aa						2222

<210> 21

<211> 2371

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 21

gcaccgcgcg	agcttggctg	cttctggggc	ctgtgtggcc	ctgtgtgtcg	gaaagatgga	60
gcaagaagcc	gagcccagag	ggcggccgcg	accctcttga	ccgagatcct	gctgctttcg	120
agccaggagc	accgtccctc	cccggattag	tgcgtacgag	cgcccagtg	cctggcccgcg	180
agagtggaa	gatccccgag	gccaggggcg	tcgtgcttcc	gcagtagtca	gtccccgtga	240
aggaaaactg	ggagtcttga	gggacccccg	actccaagcg	cgaaaacccc	ggatgggtgag	300
gagcaggcaa	atgtgcaata	ccaacatgtc	tgtacctact	gatgggtgctg	taaccacctc	360
acagattcca	gcttcggaac	aagagaccct	ggttagacca	aagccattgc	ttttgaagtt	420
attaaagtct	gttgggtgcac	aaaaagacac	ttatactatg	aaagagggtc	ttttttatct	480
tggccagtat	attatgacta	aacgattata	tgatgagaag	caacaacata	ttgtatatgt	540
ttcaaagtga	cttctaggag	atttgtttgg	cgtgccaagc	ttctctgtga	aagagcacag	600
gaaaatatat	accatgatct	acaggaactt	ggtagtagtc	aatcagcagg	aatcatcgga	660
ctcagggtaca	tctgtgagtg	agaacagggt	tcaccttgaa	ggtggggagtg	atcaaaaagga	720
ccttgtagaa	gagcttcagg	aagagaaacc	ttcatcttca	catttggttt	ctagaccatc	780
tacctcatct	agaaggagag	caattagtga	gacagaagaa	aattcagatg	aattatctgg	840
tgaacgacaa	agaaaacgcc	acaaatctga	tagtatttcc	ctttcctttg	atgaaaagctt	900
ggctctgtgt	gtaataaggg	agatatgttg	tgaagaagc	agtagcagtg	aatctacagg	960
gacgccatcg	aatccggatc	ttgatgctgg	tgtaaagtga	cattcagggtg	attggtttgga	1020
tcaggattca	gtttcagatc	agtttagtgt	agaatttgaa	gttgaatctc	tcgactcaga	1080
agattatagc	cttagtgaa	aaggacaaga	actctcagat	gaagatgatg	aggtatatca	1140
agttactgtg	tatcaggcag	gggagagtga	tacagattca	tttgaagaag	atcctgaaat	1200
ttccttagct	gactattgga	aatgcacttc	atgcaatgaa	atgaatcccc	cccttccatc	1260
acattgcaac	agatgttggg	cccttcgtga	gaattggctt	cctgaagata	aaggggaaaga	1320
taaaggggaa	atctctgaga	aagccaaact	ggaaaactca	acacaagctg	aagagggtct	1380
tgatgttcct	gattgtaaaa	aaactatagt	gaatgattcc	agagagtcac	gtgttgagga	1440
aaatgatgat	aaaattacac	aagcttcaca	atcacaagaa	agtgaagact	attctcagcc	1500
atcaacttct	agtagcatta	tttatagcag	ccaagaagat	gtgaaagagt	ttgaaaggga	1560
agaaacccaa	gacaaagaag	agagtgtgga	atctagtgtg	ccccttaatg	ccattgaacc	1620
ttgtgtgatt	tgtcaagggtc	gacctaaaaa	tgggtgcatt	gtccatggca	aaacaggaca	1680
tcttatggcc	tgctttacat	gtgcaaagaa	gctaaagaaa	aggaataaagc	cctgcccagt	1740
atgtagacaa	ccaattcaaa	tgattgtgct	aacttatctc	ccctagtgtg	cctgtctata	1800
agagaattat	atatttctaa	ctatataaac	ctaggaattt	agacaacctg	aaatttatct	1860
acatatatca	aagttagaaa	atgcctcaat	tcacatagat	ttcttctctt	tagtataatt	1920
gacctacttt	ggtagtggaa	tagtgaatac	ttactataat	ttgacttgaa	tatgtagctc	1980
atcctttaca	ccaactccta	attttaaata	atttctactc	tgtcttaaat	gagaagtact	2040
tgggtttttt	tttcttaaat	atgtatatga	catttaaatg	taacttatta	ttttttttga	2100
gaccgagtct	tgctctgtta	cccaggctgg	agtgcagtg	gtgatcttgg	ctcactgcaa	2160
gctctgccct	cccgggttc	gcaccattct	cctgcctcag	cctcccaatt	agcttggcct	2220
acagtcacat	gccaccacac	ctggctaatt	ttttgtactt	ttagtagaga	cagggtttca	2280

ccgtgttagc caggatggtc tcgatctcct gacctcgtga tccgcccacc tcggcctccc  
 aaagtgcctgg gattacaggc atgagccacc g

2340

2371

&lt;210&gt; 22

&lt;211&gt; 491

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
 synthetic construct

&lt;400&gt; 22

Met	Cys	Asn	Thr	Asn	Met	Ser	Val	Pro	Thr	Asp	Gly	Ala	Val	Thr	Thr
1				5					10					15	
Ser	Gln	Ile	Pro	Ala	Ser	Glu	Gln	Glu	Thr	Leu	Val	Arg	Pro	Lys	Pro
			20					25					30		
Leu	Leu	Leu	Lys	Leu	Leu	Lys	Ser	Val	Gly	Ala	Gln	Lys	Asp	Thr	Tyr
		35					40					45			
Thr	Met	Lys	Glu	Val	Leu	Phe	Tyr	Leu	Gly	Gln	Tyr	Ile	Met	Thr	Lys
	50					55					60				
Arg	Leu	Tyr	Asp	Glu	Lys	Gln	Gln	His	Ile	Val	Tyr	Cys	Ser	Asn	Asp
65					70					75				80	
Leu	Leu	Gly	Asp	Leu	Phe	Gly	Val	Pro	Ser	Phe	Ser	Val	Lys	Glu	His
			85					90					95		
Arg	Lys	Ile	Tyr	Thr	Met	Ile	Tyr	Arg	Asn	Leu	Val	Val	Val	Asn	Gln
			100					105					110		
Gln	Glu	Ser	Ser	Asp	Ser	Gly	Thr	Ser	Val	Ser	Glu	Asn	Arg	Cys	His
		115				120						125			
Leu	Glu	Gly	Gly	Ser	Asp	Gln	Lys	Asp	Leu	Val	Gln	Glu	Leu	Gln	Glu
	130					135					140				
Glu	Lys	Pro	Ser	Ser	Ser	His	Leu	Val	Ser	Arg	Pro	Ser	Thr	Ser	Ser
145					150					155				160	
Arg	Arg	Arg	Ala	Ile	Ser	Glu	Thr	Glu	Glu	Asn	Ser	Asp	Glu	Leu	Ser
			165					170					175		
Gly	Glu	Arg	Gln	Arg	Lys	Arg	His	Lys	Ser	Asp	Ser	Ile	Ser	Leu	Ser
		180					185					190			
Phe	Asp	Glu	Ser	Leu	Ala	Leu	Cys	Val	Ile	Arg	Glu	Ile	Cys	Cys	Glu
	195					200					205				
Arg	Ser	Ser	Ser	Ser	Glu	Ser	Thr	Gly	Thr	Pro	Ser	Asn	Pro	Asp	Leu
	210					215					220				
Asp	Ala	Gly	Val	Ser	Glu	His	Ser	Gly	Asp	Trp	Leu	Asp	Gln	Asp	Ser
225					230				235					240	
Val	Ser	Asp	Gln	Phe	Ser	Val	Glu	Phe	Glu	Val	Glu	Ser	Leu	Asp	Ser
			245					250					255		
Glu	Asp	Tyr	Ser	Leu	Ser	Glu	Glu	Gly	Gln	Glu	Leu	Ser	Asp	Glu	Asp
		260						265					270		
Asp	Glu	Val	Tyr	Gln	Val	Thr	Val	Tyr	Gln	Ala	Gly	Glu	Ser	Asp	Thr
	275					280						285			
Asp	Ser	Phe	Glu	Glu	Asp	Pro	Glu	Ile	Ser	Leu	Ala	Asp	Tyr	Trp	Lys
	290					295					300				
Cys	Thr	Ser	Cys	Asn	Glu	Met	Asn	Pro	Pro	Leu	Pro	Ser	His	Cys	Asn
305					310					315				320	
Arg	Cys	Trp	Ala	Leu	Arg	Glu	Asn	Trp	Leu	Pro	Glu	Asp	Lys	Gly	Lys
			325					330					335		
Asp	Lys	Gly	Glu	Ile	Ser	Glu	Lys	Ala	Lys	Leu	Glu	Asn	Ser	Thr	Gln
		340						345				350			
Ala	Glu	Glu	Gly	Phe	Asp	Val	Pro	Asp	Cys	Lys	Lys	Thr	Ile	Val	Asn
	355					360						365			
Asp	Ser	Arg	Glu	Ser	Cys	Val	Glu	Glu	Asn	Asp	Asp	Lys	Ile	Thr	Gln

370	375	380
Ala Ser Gln Ser Gln Glu Ser Glu Asp Tyr Ser Gln Pro Ser Thr Ser		
385	390	395
Ser Ser Ile Ile Tyr Ser Ser Gln Glu Asp Val Lys Glu Phe Glu Arg		400
	405	410
Glu Glu Thr Gln Asp Lys Glu Glu Ser Val Glu Ser Ser Leu Pro Leu		415
	420	425
Asn Ala Ile Glu Pro Cys Val Ile Cys Gln Gly Arg Pro Lys Asn Gly		430
	435	440
Cys Ile Val His Gly Lys Thr Gly His Leu Met Ala Cys Phe Thr Cys		445
	450	455
Ala Lys Lys Leu Lys Lys Arg Asn Lys Pro Cys Pro Val Cys Arg Gln		460
465	470	475
Pro Ile Gln Met Ile Val Leu Thr Tyr Phe Pro		480
	485	490

&lt;210&gt; 23

&lt;211&gt; 1599

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

&lt;400&gt; 23

gagactgtgc	cctgtccacg	gtgcctcctg	catgtcctgc	tgccctgagc	tgtcccagac	60
taggtgacag	cgtaccacgc	tgccaccatg	aatgaggtgt	ctgtcatcaa	agaaggctgg	120
ctccacaagc	gtggtgaata	catcaagacc	tggaggccac	ggtagcttct	gctgaagagc	180
gacggctcct	tcattgggta	caaggagagg	cccaggcccc	ctgatcagac	tctaccccc	240
ttaaacaact	tctccgtagc	agaatgccag	ctgatgaaga	ccgagaggcc	gcgacccaac	300
acctttgtca	tacgctgcct	gcagtggacc	acagtcatcg	agaggacctt	ccacgtggat	360
tctccagacg	agagggagga	gtggatgcgg	gccatccaga	tggtcgcaa	cagcctcaag	420
cagcgggccc	caggcgagga	ccccatggac	tacaagtgtg	gctccccccag	tgactcctcc	480
acgactgagg	agatggaagt	ggcggtcagc	aaggcacggg	ctaaagtgac	catgaatgac	540
ttcgactatc	tcaaactcct	tggcaaggga	acctttggca	aagtcatcct	ggtgcgggag	600
aaggccactg	gccgctacta	cgccatgaag	atcctgcgaa	aggaagtcac	cattgccaag	660
gatgaagtcg	ctcacacagt	caccgagagc	cgggtcctcc	agaacaccag	gcaccggttc	720
ctcactgcgc	tgaagtatgc	cttcacagac	cacgaccgcc	tgtgctttgt	gatggagtat	780
gccaacgggg	gtgagctggt	cttcacacct	tcccgggagc	gtgtcttcac	agaggagcgg	840
gcccggtttt	atggtgcaga	gattgtctcg	gctcttgagt	acttgcactc	gcgggacgtg	900
gtataccgcg	acatcaagct	ggaaaacctc	atgctggaca	aagatggcca	catcaagatc	960
actgactttg	gcctctgcaa	agagggcac	agtgcggggg	ccaccatgaa	aaccttctgt	1020
gggacccccg	agtagctggc	gcctgaggtg	ctggaggaca	atgactatgg	ccgggcccgtg	1080
gactggtggg	ggctgggtgt	ggtcatgtac	gagatgatgt	gcggccgcct	gcccttctac	1140
aaccaggacc	acgagcgctt	cttcgagctc	atcctcatgg	aagagatccg	cttcccgcgc	1200
acgctcagcc	ccgaggccaa	gtccctgctt	gctgggctgc	ttaagaagga	ccccaaagcag	1260
aggcttggtg	gggggcccag	cgatgccaag	gaggtcatgg	agcacagggt	cttcctcagc	1320
atcaactggc	aggacgtggt	ccagaagaag	ctcctgccac	ccttcaaacc	tcagggtcacg	1380
tccgaggtcg	acacaaggta	cttcgatgat	gaatttaccg	cccagtccat	cacaatcaca	1440
ccccctgacc	gctatgacag	cctgggctta	ctggagctgg	accagcggac	ccacttcccc	1500
cagttctcct	actcggccag	catccgcgag	tgagcagttc	gcccacgcag	aggacgcacg	1560
ctcgtgcca	tcaccgctgg	gtggtttttt	accctgcc			1599

&lt;210&gt; 24

&lt;211&gt; 481

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:/note =

## synthetic construct

&lt;400&gt; 24

Met	Asn	Glu	Val	Ser	Val	Ile	Lys	Glu	Gly	Trp	Leu	His	Lys	Arg	Gly
1				5					10					15	
Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	Tyr	Phe	Leu	Leu	Lys	Ser	Asp
			20					25					30		
Gly	Ser	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	Pro	Glu	Ala	Pro	Asp	Gln	Thr
		35				40						45			
Leu	Pro	Pro	Leu	Asn	Asn	Phe	Ser	Val	Ala	Glu	Cys	Gln	Leu	Met	Lys
	50				55						60				
Thr	Glu	Arg	Pro	Arg	Pro	Asn	Thr	Phe	Val	Ile	Arg	Cys	Leu	Gln	Trp
65					70					75					80
Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Asp	Ser	Pro	Asp	Glu	Arg
				85					90					95	
Glu	Glu	Trp	Met	Arg	Ala	Ile	Gln	Met	Val	Ala	Asn	Ser	Leu	Lys	Gln
			100					105					110		
Arg	Ala	Pro	Gly	Glu	Asp	Pro	Met	Asp	Tyr	Lys	Cys	Gly	Ser	Pro	Ser
		115					120					125			
Asp	Ser	Ser	Thr	Thr	Glu	Glu	Met	Glu	Val	Ala	Val	Ser	Lys	Ala	Arg
	130					135					140				
Ala	Lys	Val	Thr	Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys
145					150					155					160
Gly	Thr	Phe	Gly	Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Thr	Gly	Arg
				165					170					175	
Tyr	Tyr	Ala	Met	Lys	Ile	Leu	Arg	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp
		180						185					190		
Glu	Val	Ala	His	Thr	Val	Thr	Glu	Ser	Arg	Val	Leu	Gln	Asn	Thr	Arg
	195						200					205			
His	Pro	Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ala	Phe	Gln	Thr	His	Asp	Arg
	210					215					220				
Leu	Cys	Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His
225					230					235					240
Leu	Ser	Arg	Glu	Arg	Val	Phe	Thr	Glu	Glu	Arg	Ala	Arg	Phe	Tyr	Gly
				245					250					255	
Ala	Glu	Ile	Val	Ser	Ala	Leu	Glu	Tyr	Leu	His	Ser	Arg	Asp	Val	Val
			260					265					270		
Tyr	Arg	Asp	Ile	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His
	275						280					285			
Ile	Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Ser	Asp	Gly
	290					295					300				
Ala	Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu
305					310					315					320
Val	Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu
				325					330					335	
Gly	Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn
			340					345					350		
Gln	Asp	His	Glu	Arg	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg
		355					360					365			
Phe	Pro	Arg	Thr	Leu	Ser	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ala	Gly	Leu
	370					375					380				
Leu	Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Pro	Ser	Asp	Ala
385					390					395					400
Lys	Glu	Val	Met	Glu	His	Arg	Phe	Phe	Leu	Ser	Ile	Asn	Trp	Gln	Asp
				405					410					415	
Val	Val	Gln	Lys	Lys	Leu	Leu	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser
			420					425					430		
Glu	Val	Asp	Thr	Arg	Tyr	Phe	Asp	Asp	Glu	Phe	Thr	Ala	Gln	Ser	Ile
		435					440					445			
Thr	Ile	Thr	Pro	Pro	Asp	Arg	Tyr	Asp	Ser	Leu	Gly	Leu	Leu	Glu	Leu
	450					455					460				

Asp Gln Arg Thr His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Ile Arg  
 465 470 475 480  
 Glu

<210> 25  
 <211> 1547  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 25  
 gggagtcattc atgagcgcgtt ttaccattgt gaaagaagggt tgggttcaga agagggggaga 60  
 atatataaaa aactggaggc caagatactt ccttttgaag acagatggct cattcatagg 120  
 atataaagag aaacctcaag atgtggattt accttatccc ctcaacaact tttcagtggc 180  
 aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct 240  
 ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaagggaaga 300  
 atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat 360  
 gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac 420  
 aacccatcat aaaagaaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg 480  
 cacttttggg aaagtatttt tgggttcaga gaaggcaagt ggaaaatact atgctatgaa 540  
 gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag 600  
 cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttccagac 660  
 aaaagaccgt ttgtgtttttg tgatggaata tgtaaatggg ggcgagctgt ttttccattt 720  
 gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc 780  
 tgccttggac tatctacatt ccggaaagat tgtgtaccgt gatctcaagt tggagaatct 840  
 aatgctggac aaagatggcc acataaaaaat tacagatttt ggactttgca aagaagggat 900  
 cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagagg 960  
 gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta 1020  
 tgaaatgatg tgtgggagggt tacctttcta caaccaggac catgagaaac tttttgaatt 1080  
 aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct 1140  
 ttcagggctc ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa 1200  
 agaaattatg agacacagtt tcttctctgg agtaaactgg caagatgtat atgataaaaa 1260  
 gcttgtacct ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga 1320  
 agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggat 1380  
 ggactgcatg gacaatgaga ggcgccgca tttccctcaa ttttccctact ctgcaagtgg 1440  
 acgagaataa gtctctttca ttctgctact tcaactgtcat cttcaattta ttactgaaaa 1500  
 tgattcctgg acatcaccag tcctagctct tacacatagc aggggca 1547

<210> 26  
 <211> 479  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:/note =  
 synthetic construct

<400> 26  
 Met Ser Asp Val Thr Ile Val Lys Glu Gly Trp Val Gln Lys Arg Gly  
 1 5 10 15  
 Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp  
 20 25 30  
 Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro  
 35 40 45  
 Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr  
 50 55 60

Glu	Arg	Pro	Lys	Pro	Asn	Thr	Phe	Ile	Ile	Arg	Cys	Leu	Gln	Trp	Thr	65	70	75	80
Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Asp	Thr	Pro	Glu	Glu	Arg	Glu	85	90	95	
Glu	Trp	Thr	Glu	Ala	Ile	Gln	Ala	Val	Ala	Asp	Arg	Leu	Gln	Arg	Gln	100	105	110	
Glu	Glu	Glu	Arg	Met	Asn	Cys	Ser	Pro	Thr	Ser	Gln	Ile	Asp	Asn	Ile	115	120	125	
Gly	Glu	Glu	Glu	Met	Asp	Ala	Ser	Thr	Thr	His	His	Lys	Arg	Lys	Thr	130	135	140	
Met	Asn	Asp	Phe	Asp	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	Phe	Gly	145	150	155	160
Lys	Val	Ile	Leu	Val	Arg	Glu	Lys	Ala	Ser	Gly	Lys	Tyr	Tyr	Ala	Met	165	170	175	
Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Ile	Ala	Lys	Asp	Glu	Val	Ala	His	180	185	190	
Thr	Leu	Thr	Glu	Ser	Arg	Val	Leu	Lys	Asn	Thr	Arg	His	Pro	Phe	Leu	195	200	205	
Thr	Ser	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	Lys	Asp	Arg	Leu	Cys	Phe	Val	210	215	220	
Met	Glu	Tyr	Val	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	Arg	Glu	225	230	235	240
Arg	Val	Phe	Ser	Glu	Asp	Arg	Thr	Arg	Phe	Tyr	Gly	Ala	Glu	Ile	Val	245	250	255	
Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Gly	Lys	Ile	Val	Tyr	Arg	Asp	Leu	260	265	270	
Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	Lys	Ile	Thr	275	280	285	
Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Thr	Asp	Ala	Ala	Thr	Met	Lys	290	295	300	
Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	Leu	Glu	Asp	305	310	315	320
Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	Val	Val	Met	325	330	335	
Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	Asp	His	Glu	340	345	350	
Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Asp	Ile	Lys	Phe	Pro	Arg	Thr	355	360	365	
Leu	Ser	Ser	Asp	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	Ile	Lys	Asp	370	375	380	
Pro	Asn	Lys	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	Glu	Ile	Met	385	390	395	400
Arg	His	Ser	Phe	Phe	Ser	Gly	Val	Asn	Trp	Gln	Asp	Val	Tyr	Asp	Lys	405	410	415	
Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	Thr	Asp	Thr	420	425	430	
Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Thr	Ile	Thr	Ile	Thr	Pro	435	440	445	
Pro	Glu	Lys	Tyr	Asp	Glu	Asp	Gly	Met	Asp	Cys	Met	Asp	Asn	Glu	Arg	450	455	460	
Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Gly	Arg	Glu		465	470	475	

&lt;210&gt; 27

&lt;211&gt; 2277

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 27

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gcgaggcgag	cgcggggaag	gcaggccggc	agcccgtgtg	agcccatgc	ggcgagcgcc	120
tgcgagaagg	ggaggaggag	ccggcccgcc	gcccgcgcgc	cggggatggt	gaggaggcgg	180
cgctgcgtga	gcccagttag	gccttcgctc	gggcccgcgc	ccagctctcc	cttcctccgc	240
tcgctcgctc	cccccttccc	tctccttccc	tgcgcgcgc	gccgcgcgc	tcccatcacc	300
tcctccccgg	gctcccgcag	ccataagtag	ctgagaagga	gaaagacaag	aaaaagaaca	360
tcccttttgt	ggacccttct	gctggagttc	aggaatttca	acggtgatct	tttgactgat	420
ccaccagcct	gataaactga	tccaccaaga	gacattcccc	ccattatgaa	tgaagtagcg	480
atagtgaagg	aaggatggct	ccacaaacga	ggagaatata	tcaaaacatg	gaggccacgg	540
tattttcttt	taaagaatga	tggcacattc	attggctaca	aggaacgacc	gcaagacgtt	600
gaccaacgag	aatcaccttt	aaataacttc	tcagtagctc	agtgccagct	gatgaagaca	660
gaacgaccta	aaccaaacac	atztatcatt	agatgcctcc	agtggaccac	agtaattgaa	720
agaacatttc	atgtggagac	tccagaggag	cgggaagaat	ggacaaaagc	tatccaaact	780
gttgagacac	gcctcaagaa	acaggaggaa	gagatgatgg	attttagatc	tggttctcct	840
agtgataatt	caggtgctga	agaaatggaa	gtttctatga	caaagccaaa	acacaaagtg	900
accatgaatg	aattttgaata	ccttaagcta	ctgggaaaag	gcacttttgg	aaaggtcatt	960
ttagttaaag	aaaaagcaac	cggacggtat	tatgctatga	aaattctgaa	gaaggaagtt	1020
attgtagcaa	aggatgaagt	agcacacacg	ctgacagaaa	accgtgtttt	acagaactca	1080
cggcatccat	tcttaacagc	tttaaagtat	tcctttcaga	cacacgatcg	cttgtgtttt	1140
gttatggagt	atgctaacgg	aggggagttg	tttttccatc	tgtcgagaga	gcgtgtattt	1200
tctgaagacc	gggcgcgttt	ttatggggct	gagattgttt	cagcgttgga	ttacctgcat	1260
tcagagaaga	atgtggtgta	cagagatttg	aagctggaaa	atcttatgct	ggataaagac	1320
gggcacataa	aaattacaga	ctttggacta	tgtaaagaag	gcataaaaga	tggagcaaca	1380
atgaagactt	tctgtggcac	tccagagtat	cttgcaccag	aggtgctgga	ggataatgac	1440
tatggtcgtg	cagtggactg	gtggggatta	ggagttgtga	tgtatgaaat	gatgtgtggc	1500
cggctccctt	tctacaatca	ggaccatgaa	aagctctttg	aactcatcct	tatggaagag	1560
attagatttc	cacgcacttt	gtcacctgaa	gcaaaatctc	tcttgtcagg	tttgctgaag	1620
aaagatccta	agcaaaaggt	aggaggcgg	cctgatgatg	ccaaggagat	tatgcagcac	1680
aaattctttg	ctggcattgt	ttggcaagat	gtatacggga	agaagcttgt	acctccattt	1740
aagccacaag	ttacatctga	aacagataca	agatactttg	atgaagaatt	tacagcacag	1800
atgattacaa	tactcctcc	tgaccaagat	gacagcatgg	attgtgtaga	caatgagaga	1860
agacctcatt	ttcctcagtt	ctcctattca	gccagtggaa	ccgcttaatg	ttttgcagtg	1920
ttttccctatt	cagaaacaaa	acagactgca	ttttggggac	cttacttcaa	tggacactag	1980
agaactttct	atattatctg	aattacaac	tgtgtttgta	ttacgattta	gatgaatttc	2040
taggaagcct	cacagattct	gtatttaaaa	caattctttg	atgcattttt	gagaaggaaa	2100
acaaatccat	tcttaaaagta	ttacgtcaag	gctcttatgc	tgaacgacca	taggttttta	2160
agaatatgca	ccaaaactgt	ttacttttaga	attaattaag	gcattcaata	tcagctatag	2220
gatctaataca	ttcctgtcaa	aagtttaaga	ccaggaacct	tagagtagaa	acgaaac	2277

<210> 28

<211> 480

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =  
synthetic construct

<400> 28

Met	Asn	Glu	Val	Ala	Ile	Val	Lys	Glu	Gly	Trp	Leu	His	Lys	Arg	Gly
1			5					10						15	
Glu	Tyr	Ile	Lys	Thr	Trp	Arg	Pro	Arg	Tyr	Phe	Leu	Leu	Lys	Asn	Asp
			20					25					30		
Gly	Thr	Phe	Ile	Gly	Tyr	Lys	Glu	Arg	Pro	Gln	Asp	Val	Asp	Gln	Arg
			35				40					45			
Glu	Ser	Pro	Leu	Asn	Asn	Phe	Ser	Val	Ala	Gln	Cys	Gln	Leu	Met	Lys
			50			55					60				
Thr	Glu	Arg	Pro	Lys	Pro	Asn	Thr	Phe	Ile	Ile	Arg	Cys	Leu	Gln	Trp
65					70				75					80	



Thr	Thr	Val	Ile	Glu	Arg	Thr	Phe	His	Val	Glu	Thr	Pro	Glu	Glu	Arg	85	90	95
Glu	Glu	Trp	Thr	Lys	Ala	Ile	Gln	Thr	Val	Ala	Asp	Ser	Leu	Lys	Lys	100	105	110
Gln	Glu	Glu	Glu	Met	Met	Asp	Phe	Arg	Ser	Gly	Ser	Pro	Ser	Asp	Asn	115	120	125
Ser	Gly	Ala	Glu	Glu	Met	Glu	Val	Ser	Met	Thr	Lys	Pro	Lys	His	Lys	130	135	140
Val	Thr	Met	Asn	Glu	Phe	Glu	Tyr	Leu	Lys	Leu	Leu	Gly	Lys	Gly	Thr	145	150	155
Phe	Gly	Lys	Val	Ile	Leu	Val	Lys	Glu	Lys	Ala	Thr	Gly	Arg	Tyr	Tyr	165	170	175
Ala	Met	Lys	Ile	Leu	Lys	Lys	Glu	Val	Ile	Val	Ala	Lys	Asp	Glu	Val	180	185	190
Ala	His	Thr	Leu	Thr	Glu	Asn	Arg	Val	Leu	Gln	Asn	Ser	Arg	His	Pro	195	200	205
Phe	Leu	Thr	Ala	Leu	Lys	Tyr	Ser	Phe	Gln	Thr	His	Asp	Arg	Leu	Cys	210	215	220
Phe	Val	Met	Glu	Tyr	Ala	Asn	Gly	Gly	Glu	Leu	Phe	Phe	His	Leu	Ser	225	230	235
Arg	Glu	Arg	Val	Phe	Ser	Glu	Asp	Arg	Ala	Arg	Phe	Tyr	Gly	Ala	Glu	245	250	255
Ile	Val	Ser	Ala	Leu	Asp	Tyr	Leu	His	Ser	Glu	Lys	Asn	Val	Val	Tyr	260	265	270
Arg	Asp	Leu	Lys	Leu	Glu	Asn	Leu	Met	Leu	Asp	Lys	Asp	Gly	His	Ile	275	280	285
Lys	Ile	Thr	Asp	Phe	Gly	Leu	Cys	Lys	Glu	Gly	Ile	Lys	Asp	Gly	Ala	290	295	300
Thr	Met	Lys	Thr	Phe	Cys	Gly	Thr	Pro	Glu	Tyr	Leu	Ala	Pro	Glu	Val	305	310	315
Leu	Glu	Asp	Asn	Asp	Tyr	Gly	Arg	Ala	Val	Asp	Trp	Trp	Gly	Leu	Gly	325	330	335
Val	Val	Met	Tyr	Glu	Met	Met	Cys	Gly	Arg	Leu	Pro	Phe	Tyr	Asn	Gln	340	345	350
Asp	His	Glu	Lys	Leu	Phe	Glu	Leu	Ile	Leu	Met	Glu	Glu	Ile	Arg	Phe	355	360	365
Pro	Arg	Thr	Leu	Ser	Pro	Glu	Ala	Lys	Ser	Leu	Leu	Ser	Gly	Leu	Leu	370	375	380
Lys	Lys	Asp	Pro	Lys	Gln	Arg	Leu	Gly	Gly	Gly	Pro	Asp	Asp	Ala	Lys	385	390	395
Glu	Ile	Met	Gln	His	Lys	Phe	Phe	Ala	Gly	Ile	Val	Trp	Gln	Asp	Val	405	410	415
Tyr	Gly	Lys	Lys	Leu	Val	Pro	Pro	Phe	Lys	Pro	Gln	Val	Thr	Ser	Glu	420	425	430
Thr	Asp	Thr	Arg	Tyr	Phe	Asp	Glu	Glu	Phe	Thr	Ala	Gln	Met	Ile	Thr	435	440	445
Ile	Thr	Pro	Pro	Asp	Gln	Asp	Asp	Ser	Met	Asp	Cys	Val	Asp	Asn	Glu	450	455	460
Arg	Arg	Pro	His	Phe	Pro	Gln	Phe	Ser	Tyr	Ser	Ala	Ser	Gly	Thr	Ala	465	470	475